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     (FILE 'HOME' ENTERED AT 18:07:12 ON 24 AUG 2001)

     FILE 'MEDLINE, CAPLUS, AGRICOLA' ENTERED AT 18:07:23 ON 24 AUG 2001
L1             2 S (PSEUDOMONAS AERUGINOSA OR P AERUGINOSA OR PSEUDOMONAS) AND
(
L2             2 S (23S (5A) 5S (5A) (SPACER OR INTERGENIC)) AND PSEUDOMONAS
L3             2 S (23S (10A) 5S (10A) (SPACER OR INTERGENIC)) AND PSEUDOMONAS

     FILE 'USPATFULL, EUROPATFULL' ENTERED AT 18:11:08 ON 24 AUG 2001
L4             6 S (23S (10A) 5S (10A) (SPACER OR INTERGENIC)) AND PSEUDOMONAS
L5             6 DUP REM L4 (0 DUPLICATES REMOVED)
L6             0 S L5 NOT L3

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L5 ANSWER 2 OF 6 USPATFULL
AN 2001:29298 USPATFULL
TI Genus and species-specific identification of Legionella
IN Heidrich, Bjorn, Berlin, Germany, Federal Republic of
Robinson, Peter-Nicholas, Berlin, Germany, Federal Republic of
Tiecke, Frank, Berlin, Germany, Federal Republic of
Rolfs, Arndt, Rostock, Germany, Federal Republic of
PA Roche Diagnostics GmbH, Mannheim, Germany, Federal Republic of (non-U.S.
corporation)
PI US 6194145 B1 20010227
AI US 1996-638931 19960425 (8)
PRAI DE 1995-19515891 19950429
DT Utility
FS Granted
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Whisenant, Ethan
LREP Nikaido Marmelstein Murray & Oram, LLP.
CLMN Number of Claims: 33
ECL Exemplary Claim: 1
DRWN 5 Drawing Figure(s); 5 Drawing Page(s)
LN.CNT 1046
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Method for the genus-specific amplification of legionella and genus-specific or species-specific identification.

DE BREVET

AN 756006 EUROPATFULL ED 19970307 EW 199705 FS OS
TIEN Nucleotide sequence of the mycoplasma genitalium genome, fragments thereof, and uses thereof.
TIDE Nukleinsaeuresequenz des Mycoplasma-genitalium-Genoms, entsprechende Fragmente und ihre Verwendungen.
TIFR Sequence nucleotidique du genome de Mycoplasma genitalium, ses fragments et ses utilisations.
IN Fraser, Claire M., 9708 Medical Center Drive, Rockville, Maryland 20850, US;
Adams, Mark D., 15205 Dufief Drive, N. Potomac, Maryland, US;
Gocayne, Jeannine D., 2715 Harmon Road, Silver Springs, Maryland 20902, US;
Hutchison, Clyde A., III, 260 Edgewood Road, Chapel Hill, North Carolina 27514, US;
Smith, Hamilton O., 8222 Carrbridge Circle, Towson, Maryland 21204, US;
Venter, J. Craig, 9708 Medical Center Drive, Rockville, Maryland 20850, US;
White, Owen, 886 Quince Orchard Blvd., Apt. 202, Gaithersburg, Maryland 20878, US
PA THE INSTITUTE FOR GENOMIC RESEARCH, 9712 Medical Center Drive, Rockville, Maryland 20850, US;
THE JOHNS HOPKINS UNIVERSITY, 720 Rutland Avenue, Baltimore, MD 21205, US;
THE UNIVERSITY OF NORTH CAROLINA AT CHAPEL HILL, CB No. 4105, 308 Bynum Hall, Chapel Hill, North Carolina 27599-4105, US
PAN 2152390; 348140; 751085
AG VOSSIUS & PARTNER, Siebertstrasse 4, 81675 Muenchen, DE
AGN 100314
OS ESP1997006 EP 0756006 A2 970129
SO Wila-EPZ-1997-H05-T1a
DT Patent
LA Anmeldung in Englisch; Veroeffentlichung in Englisch
DS R AT; R BE; R CH; R DE; R DK; R ES; R FI; R FR; R GB; R GR; R IE; R IT; R LI; R LU; R MC; R NL; R PT; R SE
PIT EPA2 EUROPAEISCHE PATENTANMELDUNG
PI EP 756006 A2 19970129
OD 19970129
AI EP 1996-109204 19960607
PRAI US 1995-488018 19950607
US 1995-473545 19950607
US 1995-545528 19951019
ABEN The present invention provides the nucleotide sequence of the entire genome of Mycoplasma genitalium, SEQ ID NO:1. The present invention further provides the sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use. In addition to the entire genomic sequence, the present invention identifies protein encoding fragments of the genome, and identifies, by position relative to two (2) genes known to flank the origin of replication, any regulatory elements which modulate the expression of the protein encoding fragments of the Mycoplasma genitalium genome.

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     (FILE 'HOME' ENTERED AT 18:58:20 ON 24 AUG 2001)

     FILE 'MEDLINE, CAPLUS' ENTERED AT 18:58:28 ON 24 AUG 2001
L1            38 S (5S (5A) 23S (5A) (SPACER OR INTERGENIC)) (P) (VARIABLE OR
PO
L2            22 DUP REM L1 (16 DUPLICATES REMOVED)
L3             1 S L2 AND BACTERIA
L4             0 S L2 AND GRAM NEGATIVE
L5             0 S L2 AND PSEUDOMONAS
L6            37 S (5S (5A) 23S (5A) (SPACER OR INTERGENIC)) (P) (PROBE? OR
PRIM
L7            29 S L6 NOT L2
L8            23 DUP REM L7 (6 DUPLICATES REMOVED)

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L2 ANSWER 19 OF 22 CAPLUS COPYRIGHT 2001 ACS
AN 1993:532907 CAPLUS
DN 119:132907
TI Method for the identification of microorganisms by the utilization of directed and arbitrary DNA amplification
IN Jensen, Mark Anton; Straus, Neil Alexander
PA du Pont de Nemours, E. I., and Co., USA
SO PCT Int. Appl., 51 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9311264	A1	19930610	WO 1992-US10217	19921202
	W: AU, BR, CA, JP, RU, UA				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	AU 9331485	A1	19930628	AU 1993-31485	19921202
	EP 620862	A1	19941026	EP 1992-925423	19921202
	EP 620862	B1	19980429		
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
	AT 165622	E	19980515	AT 1992-925423	19921202
	ES 2114957	T3	19980616	ES 1992-925423	19921202
	LV 10311	B	19950420	LV 1993-347	19930514
	US 5753467	A	19980519	US 1996-701290	19960822
PRAI	US 1991-803302		19911204		
	WO 1992-US10217		19921202		
	US 1994-281496		19940727		

AB The title method comprises first isolating genomic DNA from the microorganism. **Variable spacer** regions lying between 16S and **23S** rRNA and 23S and **5S** rRNA genes are amplified. The amplification process is carried out in order to amplify only these **variable** spacer regions or to amplify both these regions and arbitrary genomic regions in conjunction with the **variable** regions. The resulting amplified DNA fragments are **polymorphic** with respect to both size and no. in a manner which is specific to species, serotype, and strain. The distribution of **polymorphic** fragments is analyzed and compared to an established database to det. the species, serotype, and strain of the microorganism. The use of 15-mer PCR primers for amplification of **variable** sequences between the 16S and 23S rRNA genes for identification of microbial species was demonstrated. 11-Mer subsequences of the primers were used to amplify arbitrary genomic regions as well as the intergenic **variable** regions to further identify serotype and strain.